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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE
(Case No. 02-076)

PATENT

In re Application of: Elliott et al.

Serial No.: 10/076,260

Filed: February 14, 2002

For: G-Protein Coupled Receptor
Molecules and Uses Thereof

Before the Examiner: F. Hamud

Group Art Unit: 1647

Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

Sir:

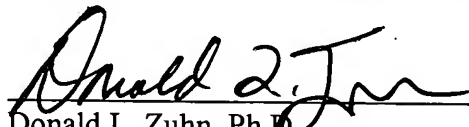
TRANSMITTAL LETTER

1. We are transmitting herewith the attached papers for the above-described patent application:
Response to Restriction Requirement and return postcard.
2. GENERAL AUTHORIZATION TO CHARGE OR CREDIT FEES: Please charge any additional fees or credit any overpayment to Deposit Account No. 13-2490.
3. CERTIFICATE OF MAILING UNDER 37 C.F.R. § 1.8: The undersigned hereby certifies that this Transmittal Letter and the papers, as described in paragraph 1, are being deposited with the United States Postal Service with sufficient postage as first class mail in an envelope addressed to: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450, on April 26, 2004.

Respectfully submitted,
McDonnell Boehnen Hulbert & Berghoff

Dated: April 26, 2004

By:


Donald L. Zuhn, Ph.D.
Reg. No. 48,710



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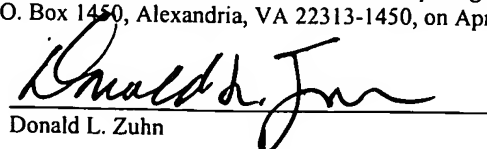
RESPONSE TO RESTRICTION REQUIREMENT MAILED MARCH 25, 2004

Responsive to the Restriction Requirement mailed March 25, 2004, Applicants elect to prosecute claims 1-8, 10, 11, 43-45, 56, and 57, designated as the invention of Group I by the Action, which the Action states are drawn to an isolated nucleic acid molecule comprising a specific nucleotide sequence. The Action also asserts that the claims of Group I-X recite a multitude of nucleic acid sequences and polypeptide sequences that constitutes a recitation of an implied, mis-joined Markush group containing multiple independent and distinct inventions, and that each of the nucleic acids is independent and distinct because no common structural or functional properties are shared. To the extent that Applicants understand this assertion, Applicants elect to prosecute claims directed to nucleic acid molecules encoding human GPCR polypeptides, with traverse.

Applicants first request clarification regarding the Action's assertion that the claims of Group I-X recite a multitude of nucleic acid sequences and polypeptide sequences that constitutes a recitation of an implied, mis-joined Markush group containing multiple independent and distinct inventions, and that each of the nucleic acids is independent and distinct because no common structural or functional properties are shared. Assuming that Applicants have correctly interpreted

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Donald L. Zuhn

the instant Action as requiring an election of a genus of nucleic acid molecules encoding human, murine, or rat GPCR polypeptides, Applicants elect to prosecute claims directed to nucleic acid molecules encoding human GPCR polypeptides (*i.e.*, the nucleic acid molecule of SEQ ID NO: 1, nucleic acid molecules encoding the polypeptide of SEQ ID NO: 2, and nucleic acid molecules encoding variants and fragments of the polypeptide of SEQ ID NO: 2), with traverse. The basis for Applicants' traversal of the requirement is as follows. Applicants respectfully submit that because the genus of nucleic acid molecules encoding human, murine, and rat GPCR polypeptides shares common structural properties and substantial amino acid identity and similarity, the members of this genus do not constitute multiple independent and distinct inventions.

Applicants note that the instant application teaches nucleic acid molecules encoding human, murine, and rat GPCR polypeptides, and contend that in view of the substantial amino acid identity and similarity shared by these polypeptides (Exhibit A), one of ordinary skill in the art would clearly recognize that the human, murine, and rat GPCR polypeptides taught in the instant application are orthologs. Applicants also note that the human and murine GPCR polypeptides taught in the instant application share 78% identity and 85% similarity (Exhibit B), the human and rat GPCR polypeptides share 78% identity and 86% similarity (Exhibit C), and the murine and rat GPCR polypeptides share 90% identity and 93% similarity. Moreover, as disclosed in Figure 4 of the instant application, the human, murine, and rat GPCR polypeptides also share common structural properties in that each protein possesses seven transmembrane domains. The ClustalW sequence alignments shown in Exhibits B-D were performed using the application MacVector 7.1.1 (Accelrys, Cambridge, UK; <http://www.accelrys.com>) at the default settings.

Applicants respectfully submit that because the genus of nucleic acid molecules encoding human, murine, and rat GPCR polypeptides taught in the instant application shares substantial sequence identity and similarity, and therefore, share, rather than lack, common structural properties, the members of this genus do not constitute multiple independent and distinct inventions. Applicants, therefore, respectfully request examination of claims directed to nucleic acid molecules encoding human, murine, and rat GPCR polypeptides.

Applicants do not believe that any additional fee is required. However, the Commissioner is authorized to charge any deficiency to Deposit Account No. 13-2490. If Examiner Hamud believes

it to be helpful, the Examiner is invited to contact the undersigned representative by telephone at 312-913-0001.

Respectfully submitted,
McDonnell Boehnen Hulbert & Berghoff

Dated: April 26, 2004

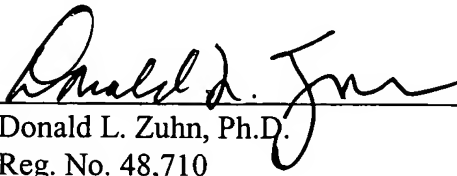
By: 
Donald L. Zuhn, Ph.D.
Reg. No. 48,710

EXHIBIT A

hul:PCR
mul:PCR
rs:PCR

M P V L S P T A M D N G S C C L I E G E P I S Q V M P P L L
 M L F L S P S A M D N G S C C L I E G E P I T Q V M P P L L
 M L S P . A M D N G S C C L I E G E P I S Q V M P P L L

hul:PCR
mul:PCR
rs:PCR

I V A F V L G A L G N G V A L C G F C F H M K T V K P S T V
 I L V F V L G A L G N G I A L C G F C F H M K T V K S S T I
 I L A F L L G A L G N G L A L C G F C F H M K T V K S S T I
 I L A F V L G A L G N G . A L C G F C F H M K T V K S S T I

hul:PCR
mul:PCR
rs:PCR

Y L F N L A V A D F L L M I C L P F R T D Y Y L R R R H V A
 Y L F N L A V A D F L L M I C L P L R T D Y Y L R R R H V I
 Y L F N L A V A D F L L M I C L P L R T D Y Y L R R R H V I
 Y L F N L A V A D F L L M I C L P L R T D Y Y L R R R H W I

hul:PCR
mul:PCR
rs:PCR

F G D I P C R V G L F T L A M N R A G S I V F L T V V A A D
 F G D I A C R L V L F K L A M N R A G S I V F L T V V A V D
 L G D I P C R L V L F M L A M N R A G S I V F L T V V A V D
 F G D I P C R L V L F L A M N R A G S I V F L T V V A V D

hul:PCR
mul:PCR
rs:PCR

R Y F K V V H P H H A V N T I S T I R V A A G I V C T L V A T
 R Y F K V V H P H H M V N A I S N R T A A A T A C V L V T L
 R Y F K V V H P H H M V N A I S N R T A A A I V C V L V T L
 R Y F K V V H P H H M V N A I S N R T A A A I V C V L W T L

hul:PCR
mul:PCR
rs:PCR

V I L G T V Y L L L E N H L C V Q E T A V S C E S F I M E S
 V I L G T V Y L L M E S H L C V Q G T L S S C E S F I M E S
 V I L G T V Y L L M E S H L C V R G M V S S C E S F I M E S
 V I L G T V Y L L M E S H L C V Q G T . S S C E S F I M E S

	190	200	210
hUGPCR	ANGVHDIMFQLEFFMPLGIILFCSEFKIVWS		
muGPCR	ANGVHDVMFQLEFFLPLTIILFCSEVN>VVWS		
rsGPCR	ANGVHDIMFQLEFFLPLTIILFCSEFKVVWS		
	ANGVHDIMFQLEFFLPLTIILFCSEFKVVWS		

	220	230	240
hUGPCR	LRRRQQQLARQARMKKATRFIMVVAIVFITC		
muGPCR	LRRRQQQLTRQARMRRATRFIMVVASVFITC		
rsGPCR	LRQRQQQLTRQARMRRATRFIMVVASVFITC		
	LRRRQQQLTRQARMRRATRFIMVVASVFITC		

	250	260	270
hUGPCR	YLPSSVSAARLYFLWTVPSACDPSVHGALHI		
muGPCR	YLPSSVLARLYFLWTVPTSACDPSVHTALHV		
rsGPCR	YLPSSVLARLYFLWTVPSACDPSVHIALHV		
	YLPSSVLARLYFLWTVPSACDPSVHIALHV		

	280	290	300
hUGPCR	TLSFTYMNNSMLDPLVYYFSSSPSPKFFYNKL		
muGPCR	TLSFTYLNNSMLDPLVYYFSSSPSLPKFFYAKL		
rsGPCR	TLSLTLYLNNSMLDPLVYYFSSSPSPKFFYAKL		
	TLSFTYLNNSMLDPLVYYFSSSPSPKFFYAKL		

	310	320	330
hUGPCR	KICSLKPKQPGHSKTQRPEEMPISNLGRRS		
muGPCR	TICSLKPKRPGRTRRSEEMPISNLCSEKS		
rsGPCR	KIRSLKPRRPGRSQARRSEEMPISNLCSEKS		
	KICSLKPKRPGRSKTRRSEEMPISNLCSEKS		

	340	350	360
hUGPCR	CISVANSEFQSQSDGQWDPHIV>EW		
muGPCR	SIDGANRSQRPSDGGQWDLQVC		
rsGPCR	STDVANS>SQRPSDGGQWG>LQVC		
	SIDVANSSQRPSDGGQWDLQVCEWH		

EXHIBIT B

1. huGPCR vs. muGPCR

Aligned Length = 354 Gaps = 0
Identities = 276 (78%) Similarities = 26 (7%)

```
huGPCR    1      MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCF  42
muGPCR    1      MPVLSPTAMDNGSCCLIEGEPISQVMPPLLILVFLGALGNGIALCGFCF  50
          * ***** ***. *****. *****.*****

huGPCR    43      HMKTWKPSTVYLFNLAVADFLLMICLPFRTDYLLRRRHWAFGDIPCRVGL  92
muGPCR    51      HMKTWKSSTIYLFNLAVADFLLMICLPLRTDYLLRRRHWIFGDIACRLVL 100
          ***** **.****** ***** ***** **.*

huGPCR    93      FTLAMNRAGSIVFLTVVAADRYFKVVPHHAVNTISTRVAAGIVCTLWAL 142
muGPCR   101      FKLAMNRAGSIVFLTVVAVDRYFKVVPHHVMNAISNRTAAATACVLWTL 150
          * ***** ***** **.*.* **  * **.*

huGPCR   143      VILGTVYLLLENHLCVQETAVSCSFIMESANGWHDIMFQLEFFMPLGII  192
muGPCR   151      VILGTVYLLMESHLCVQGTLSFIMESANGWHDVMFQLEFFLPLTII  200
          *****.* ***** * *****.*****.* **

huGPCR   193      LFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSARLY  242
muGPCR   201      LFCSVNVVWSLRRRQQLTRQARMRRATRFIMVVASVFITCYLPSVLARLY  250
          *****.*****.*****.***** *****

huGPCR   243      FLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKL  292
muGPCR   251      FLWTVPTSACDPSVHTALHVTLSTYLNMLDPLVYYFSSPSLPKFYAKL  300
          *****.***** ***.*****.***** *****

huGPCR   293      KICSLKPKQPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHI  342
muGPCR   301      TICSLKPKRPGRTKTRRSEEMPISNLCSKSSIDGANRSQRPSDGQWDLQV  350
          *****.*.*.*.* ***** .*. * * ***** ..

huGPCR   343      VEWH  346
muGPCR   351      C      351
```


EXHIBIT C

2. huGPCR vs. raGPCR

Aligned Length = 354 Gaps = 0
Identities = 276 (78%) Similarities = 30 (8%)

```
huGPCR   1      MYNGSCCRIEGDTISQVMPPLLIVAFVLGALGNGVALCGFCF  42
raGPCR   1  MLFLSPSAMDNGSCCLIEGEPITQVMPPLLILAFLLGALGNGLALCGFCF  50
          * ***** ** . *.*****.***.*****.*****

huGPCR   43  HMKTWKPSTVYLFNLAVADFLLMICLPFRTDYLLRRRHWAFGDIPCRVGL  92
raGPCR   51  HMKTWKSSTIYLFNLAVADFLLMICLPLRTDYLLRRRHWILGDIPCRLVL 100
          ***** ** .*****.*****.*****.*****. *

huGPCR   93  FTLAMNRAGSIVFLTVVAADRYFKVVPHPHAVNTISTRVAAGIVCTLWAL 142
raGPCR  101  FMLAMNRAGSIVFLTVVAVDRYFKVVPHPHMVNAISNRTAAAIVCVLWTL 150
          * *****.*****.*****.***.***.***.***.***

huGPCR  143  VILGTVYLLLENHLCVQETAVSCSFIMESANGWHDIMFQLEFFMPLGII  192
raGPCR  151  VILGTVYLLMESHLCVRGMVSSCSFIMESANGWHDIMFQLEFFLPLTII  200
          *****.* ****. *****.*****.*** **

huGPCR  193  LFCSFKIVWSLRRRQQLARQARMKKATRFIMVVAIVFITCYLPSVSARLY  242
raGPCR  201  LFCSFKVWWSLRQRQQLTRQARMRRATRFIMVVASVFITCYLPSVLARLY  250
          *****.*****.*****.*****.*****.***** *****

huGPCR  243  FLWTVPSSACDPSVHGALHITLSFTYMNSMLDPLVYYFSSPSFPKFYNKL  292
raGPCR  251  FLWTVPSSACDPSVHIALHVTLSTLYLNSMLDPLVYYFSSPSFPKFYAKL  300
          *****.*****.***.*** ** .*****.*****.***** **

huGPCR  293  KICSLKPKQPGHSKTQRPEEMPISNLGRRSCISVANSFQSQSDGQWDPHI  342
raGPCR  301  KIRSLKPRRPGRSQARRSEEMPISNLCKSSTDVVNSSQRPSDGQWGLQV  350
          ** *****.***.***.*** ***** *.*. * * * * ***** ..

huGPCR  343  VEWH 346
raGPCR  351  C 351
```

EXHIBIT D

3. muGPCR vs. raGPCR

Aligned Length = 351 Gaps = 0
Identities = 316 (90%) Similarities = 13 (3%)

```
muGPCR   1 MPVLSPTAMDNGSCCLIEGEPISQVMPPLLILVFLGALGNGIALCGFCF  50
raGPCR   1 MLFLSPSAMDNGSCCLIEGEPITQVMPPLLILAFLLGALGNGIALCGFCF  50
          *   ***.*****.*****.***** * .*****.*****

muGPCR   51 HMKTWKSSTIYLFNLAVADFLLMICLPLRTDYLLRRRHWFIDGDIACRLVL 100
raGPCR   51 HMKTWKSSTIYLFNLAVADFLLMICLPLRTDYLLRRRHWFIDGDIACRLVL 100
          *****

muGPCR  101 FKLAMNRAGSIVFLTVVAVDRYFKVVPHPHMVNAISNRTAAATACVLWTL 150
raGPCR  101 FKLAMNRAGSIVFLTVVAVDRYFKVVPHPHMVNAISNRTAAATACVLWTL 150
          * *****

muGPCR  151 VILGTVYLLMESHLCVQGTLSSECFIMESANGWHDVDFQLEFFLPLTII 200
raGPCR  151 VILGTVYLLMESHLCVQGTLSSECFIMESANGWHDVDFQLEFFLPLTII 200
          *****

muGPCR  201 LFCSVNVVWSLRRRQQLTRQARMRRATRFIMVVASVFITCYLPSVLARLY 250
raGPCR  201 LFCSVNVVWSLRRRQQLTRQARMRRATRFIMVVASVFITCYLPSVLARLY 250
          *****

muGPCR  251 FLWTVPTSACDPSVHTALHVTLSFTYLNMLDPLVYFSSPSLPKFYAKL 300
raGPCR  251 FLWTVPTSACDPSVHTALHVTLSFTYLNMLDPLVYFSSPSLPKFYAKL 300
          *****

muGPCR  301 TICSLKPKRPGRTKTRRSEEMPISNLCSKSSIDGANRSQRPSDGQWDLQV 350
raGPCR  301 KIRSLKPKRPGRSQARRSEEMPISNLCSKSSIDGANRSQRPSDGQWDLQV 350
          * ****.*****.***** ***** * * *****

muGPCR  351 C 351
raGPCR  351 C 351
          *
```